

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/559,986  
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IFWO

## RAW SEQUENCE LISTING

DATE: 09/20/2006

PATENT APPLICATION: US/10/559,986

TIME: 10:53:24

Input Set : E:\PAT 60100W-1 Sequence Listing.txt

Output Set: N:\CRF4\09202006\J559986.raw

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3 <110> APPLICANT: Nestec S.A.; Cornell Research Foundation, Inc.
5 <120> TITLE OF INVENTION: Modulation Of Coffee Flavour Precursor Levels In Green
Coffee Grains
7 <130> FILE REFERENCE: PAT 60100W-1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,986
C--> 10 <141> CURRENT FILING DATE: 2005-12-08
12 <150> PRIOR APPLICATION NUMBER: EP 03394056.0
13 <151> PRIOR FILING DATE: 2003-06-20
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1543
22 <212> TYPE: DNA
23 <213> ORGANISM: Coffea canephora
25 <220> FEATURE:
26 <221> NAME/KEY: mRNA
27 <222> LOCATION: (1)..(1543)
28 <223> OTHER INFORMATION: mRNA
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (122)..(1315)
33 <223> OTHER INFORMATION: CDS
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37 ggggtccaaaa ccaccgtcca agagaggagc agactgcaga gtgatacata caggcacaaaa      120
38 g atg atg atg aca agc gga ggt ctg atg cta acc tgc act ctg gct att      169
39 Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile
40 1 5 10 15
41 acc ctc tta tcc tgc gca ctc atc tct tca acc act ttc caa cat gaa      217
42 Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu
43 20 25 30
44 att cag tat cga gta caa gac ccg tta atg ata cgc caa gtc acc gac      265
45 Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp
46 35 40 45
47 aat cac cac cac cgc cac cac cca ggt agg tct tct gca aac cat cgt      313
48 Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg
49 50 55 60
50 cta ctg ggc acc acc aca gag gtt cac ttc aag tcc ttc gtg gag gag      361
51 Leu Leu Gly Thr Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu
52 65 70 75 80
53 tac gag aaa act tac tct acg cac gag gag tac gtg cac cgc ctg ggg      409
54 Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly
55 85 90 95
56 att ttc gcc aag aac ctc atc aag gcc gcg gag cac cag gcc atg gac      457

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57 Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp
58          100          105          110
59 ccc tcc gca atc cac ggc gtc acc cag ttc tct gat ctc acc gag gag      505
60 Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu
61          115          120          125
62 gag ttt gag gct acg tac atg ggc ctt aaa ggt ggc gct gga gtt ggt      553
63 Glu Phe Glu Ala Thr Tyr Met Gly Leu Lys Gly Gly Ala Gly Val Gly
64          130          135          140
65 ggg acc acc cag ctg ggg aaa gat gat ggg gat gag agt gca gca gag      601
66 Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu
67 145          150          155          160
68 gtg atg atg gat gta tct gat ttg ccg gag agt ttt gat tgg aga gaa      649
69 Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu
70          165          170          175
71 aaa ggt gct gtg acc gaa gtg aag acg cag gga aga tgt gga tcg tgt      697
72 Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys
73          180          185          190
74 tgg gct ttt agt aca act gga gct att gaa gga gct aat ttc att gca      745
75 Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala
76          195          200          205
77 act ggc aag ctt ctc agc cta agt gaa cag cag ctt gtg gat tgt gat      793
78 Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp
79          210          215          220
80 cat atg tgt gat tta aaa gaa aaa gat gac tgt gat gat gga tgc tcc      841
81 His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser
82 225          230          235          240
83 gga ggc cta atg aca act gct ttc aac tac ttg ata gag gca gga ggt      889
84 Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly
85          245          250          255
86 ata gag gag gag gta acc tat ccc tac act ggg aaa cgc gga gaa tgc      937
87 Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys
88          260          265          270
89 aaa ttc aat cct gag aaa gtt gcg gtg aaa gtg cgg aat ttc gca aaa      985
90 Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys
91          275          280          285
92 atc cct gag gat gag agt caa att gct gcc aat gta gtg cat aat ggc      1033
93 Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly
94          290          295          300
95 ccg ctt gct att gga ttg aat gcg gta ttc atg caa act tac atc ggg      1081
96 Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly
97 305          310          315          320
98 ggt gtg tca tgt cct ctt att tgt gac aaa aag agg atc aac cat ggt      1129
99 Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly
100          325          330          335
101 gtt ctt ctt gtg ggc tat ggt tct aga ggc ttc tca atc ctt agg ctt      1177
102 Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu
103          340          345          350
104 ggc tac aag cca tac tgg att atc aag aac tca tgg ggg aag cgt tgg      1225
105 Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp

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106          355          360          365
107 ggc gaa cat ggt tgc tac cgg ctt tgt cga ggg cac aac atg tgt gga      1273
108 Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly
109          370          375          380
110 atg agc aca atg gtt tca gct gtg gtg aca cag acc tct tga      1315
111 Met Ser Thr Met Val Ser Ala Val Val Thr Gln Thr Ser
112 385          390          395
113 taccaaaaaca tctctgctct tcagaggttg tatacaaggt ggtttgctct tggaagatct      1375
114 tatcatgttt tcgaaatatt taggtttgta taatatgaag ggtagagagt aataagaacc      1435
115 aaacaaaagt tcaggcctgt ttctgatagg aatggaatat gatcggagtc atttgttact      1495
116 ggatcacaaa aaaaaatcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1543
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 397
121 <212> TYPE: PRT
122 <213> ORGANISM: Coffea canephora
124 <400> SEQUENCE: 2
125 Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile
126 1          5          10          15
127 Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu
128          20          25          30
129 Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp
130          35          40          45
131 Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg
132          50          55          60
133 Leu Leu Gly Thr Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu
134 65          70          75          80
135 Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly
136          85          90          95
137 Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp
138          100          105          110
139 Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu
140          115          120          125
141 Glu Phe Glu Ala Thr Tyr Met Gly Leu Lys Gly Gly Ala Gly Val Gly
142          130          135          140
143 Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu
144 145          150          155          160
145 Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu
146          165          170          175
147 Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys
148          180          185          190
149 Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala
150          195          200          205
151 Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp
152          210          215          220
153 His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser
154 225          230          235          240
155 Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly
156          245          250          255
157 Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys

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158          260          265          270
159 Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys
160          275          280          285
161 Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly
162          290          295          300
163 Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly
164 305          310          315          320
165 Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly
166          325          330          335
167 Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu
168          340          345          350
169 Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp
170          355          360          365
171 Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly
172          370          375          380
173 Met Ser Thr Met Val Ser Ala Val Val Thr Gln Thr Ser
174 385          390          395
177 <210> SEQ ID NO: 3
178 <211> LENGTH: 726
179 <212> TYPE: DNA
180 <213> ORGANISM: Coffea canephora
182 <220> FEATURE:
183 <221> NAME/KEY: mRNA
184 <222> LOCATION: (1)..(726)
185 <223> OTHER INFORMATION: mRNA
187 <220> FEATURE:
188 <221> NAME/KEY: CDS
189 <222> LOCATION: (79)..(498)
190 <223> OTHER INFORMATION: CDS
192 <400> SEQUENCE: 3
193 ggcgcaacaa acattgaaag aaaatcaaga acccaaaaaa accccacaag aaaaaaagaa      60
194 aaagaagaag aaaagcca atg gca aaa cca tgc tca tct cta ctc aca ctt      111
195          Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu
196          1          5          10
197 cct tcc ttt ctt ctg atc ttt ttc att ctt gca cta ttt tcc acc acc      159
198 Pro Ser Phe Leu Leu Ile Phe Phe Ile Leu Ala Leu Phe Ser Thr Thr
199          15          20          25
200 ctc caa gtt aat gcc ttg gga agg aaa gtg gga gca agg gag aag att      207
201 Leu Gln Val Asn Ala Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile
202          30          35          40
203 gag gat gtg aag agc aac aaa gaa gtt caa gaa ctt ggg gaa tat tgt      255
204 Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys
205          45          50          55
206 gtt tct gag tac aac aag agt ttg cgg aag aag aac aac gaa agt ggt      303
207 Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly
208 60          65          70          75
209 gct cct ata atc ttc aca tct gtg gtg gag gct gag aag cag gtg gtt      351
210 Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val
211          80          85          90

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212 gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg      399
213 Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly
214          95                      100                      105
215 gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat      447
216 Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His
217          110                      115                      120
218 act aag cca agg cag ttg ctc aag ttc tcc cct tcc cct gcc act aaa      495
219 Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys
220          125                      130                      135
221 tga agaagaaaat gttgaaaaag ttggaactgt ttgggagatc taatctgatg      548
222 attattagta cctttcagtg caaattctct ttgctgttaa gtgttcggtt tttttttttt      608
223 ccctgtgtct atttatgacc gtggtcacga tgatatgggtg tatgatccag taataattaa      668
224 aatctgttgc ataaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      726
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 139
229 <212> TYPE: PRT
230 <213> ORGANISM: Coffea canephora
232 <400> SEQUENCE: 4
233 Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu Pro Ser Phe Leu Leu
234 1          5                      10                      15
235 Ile Phe Phe Ile Leu Ala Leu Phe Ser Thr Thr Leu Gln Val Asn Ala
236          20                      25                      30
237 Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile Glu Asp Val Lys Ser
238          35                      40                      45
239 Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys Val Ser Glu Tyr Asn
240          50                      55                      60
241 Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly Ala Pro Ile Ile Phe
242 65          70                      75                      80
243 Thr Ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr
244          85                      90                      95
245 Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr
246          100                     105                     110
247 Asp Ala Ile Val Val Val Arg Pro Trp Val His Thr Lys Pro Arg Gln
248          115                     120                     125
249 Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys
250          130                     135
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 2282
255 <212> TYPE: DNA
256 <213> ORGANISM: Coffea canephora
258 <220> FEATURE:
259 <221> NAME/KEY: mRNA
260 <222> LOCATION: (1)..(2282)
261 <223> OTHER INFORMATION: mRNA
263 <220> FEATURE:
264 <221> NAME/KEY: CDS
265 <222> LOCATION: (439)..(1731)
266 <223> OTHER INFORMATION: CDS
268 <400> SEQUENCE: 5

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**VERIFICATION SUMMARY**

DATE: 09/20/2006

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TIME: 10:53:25

Input Set : E:\PAT 60100W-1 Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date